Brain Tumor Segmentation Using U-Net

Introduction

Brain Tumor Segmentation from Magnetic Resonance Imaging (MRI) is a vital step in clinical oncology. However, the current standard of manual segmentation by radiologists is time-consuming and prone to considerable inter-observer variability, compromising the consistency and speed required for urgent patient care.

We propose an automated pipeline that leverages the U-Net Deep Learning architecture. Crucially, our methodology is empowered by using image processing for enhance the detection and analysis of brain tumors **by improving image quality, segmenting tumor regions, classifying tumor types, and enabling accurate measurement and treatment planning.** This combined approach is engineered to significantly reduce diagnostic time and substantially increase the accuracy of tumor detection, ensuring robust and reliable clinical results.

Objective

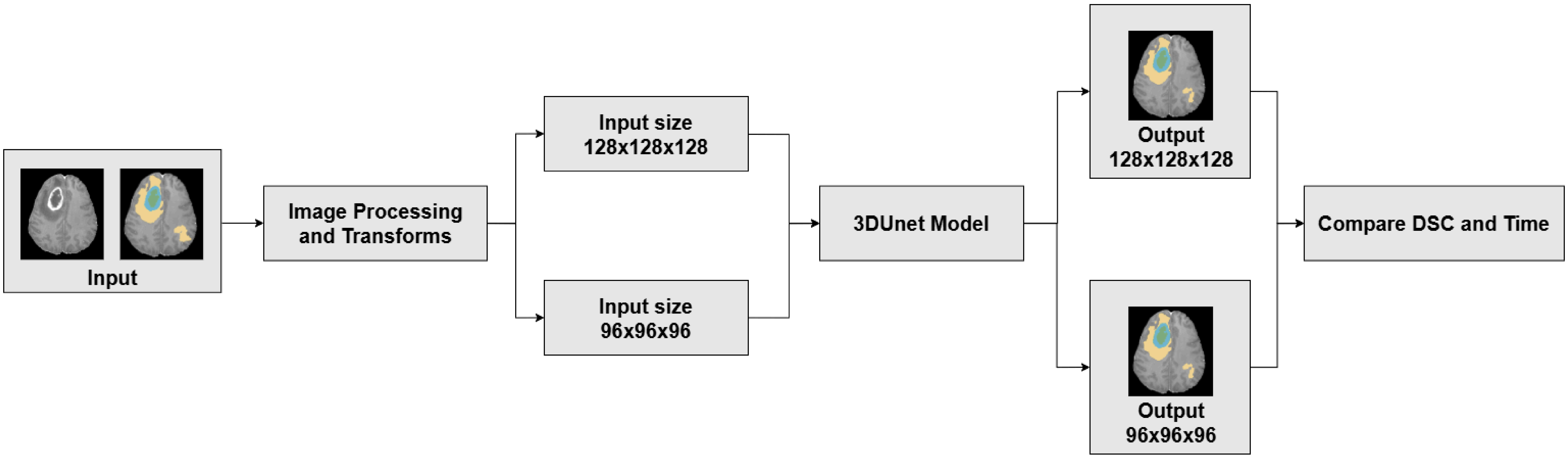
The reliability and performance of the segmentation result are fundamentally influenced by the upstream Image Processing steps.

The objectives of this research are to:

- Determine Image Processing Impact: Systematically investigate how varying the Input Patch Dimension affects the model's learning capacity and final segmentation Result.
- Evaluate Input Size Effects: Analyze the consequences of different input sizes on the model's Generalization capability and its computational Efficiency.

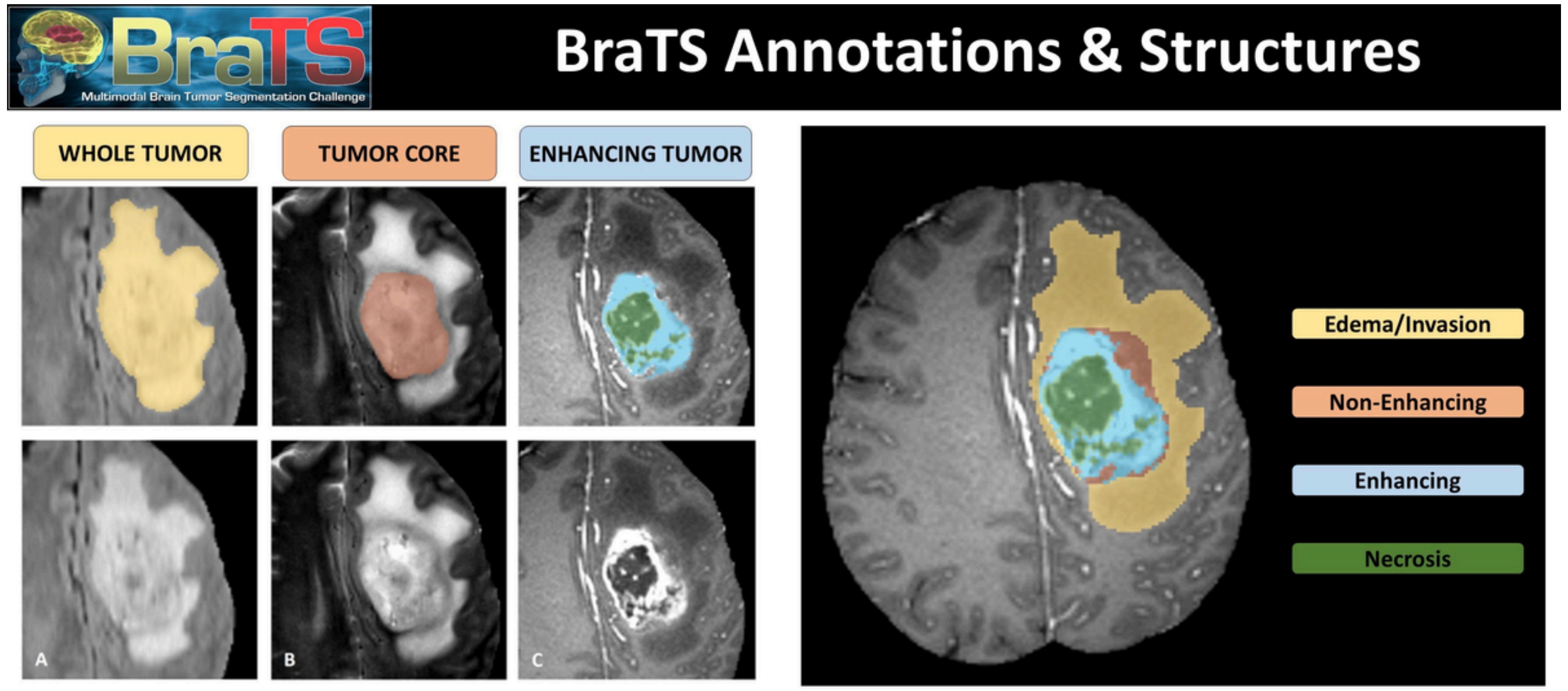
Methodology

Workflow



Methodology

Dataset

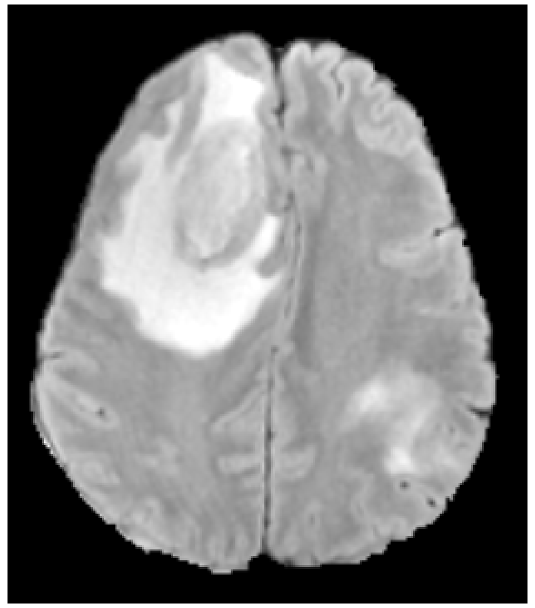


The data utilized for this research is sourced from the widely recognized MICCAI **Brain Tumor Segmentation (BraTS) 2020 Challenge Dataset**. This standardized dataset consists of multimodal volumetric Magnetic Resonance Imaging (MRI) scans of gliomas.

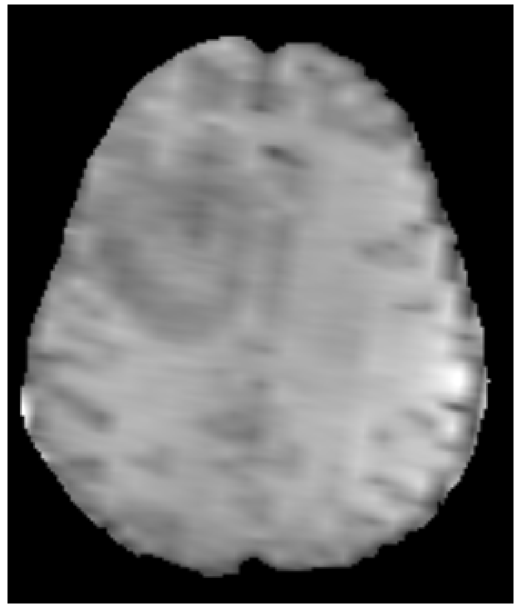
- Total Data Volume: The dataset comprises 494 total volumes (369 for training and 125 for validation).
- Imaging Modalities: Each patient case includes four sequences: T1-weighted (T1), T1-weighted with contrast enhancement (T1-CE), T2-weighted (T2), and Fluid Attenuated Inversion Recovery (FLAIR).
- Original Labels: The ground truth manual segmentations are provided using specific labels:
  - Label 0: Background / Healthy Tissue.
  - Label 1: Necrotic Core (NCR).
  - Label 2: Peritumoral Edema (ED).
  - Label 4: Enhancing Tumor (ET).

Methodology

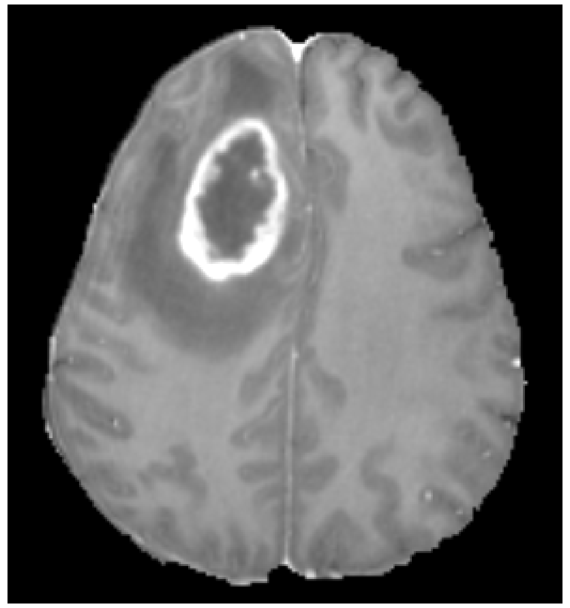
Dataset



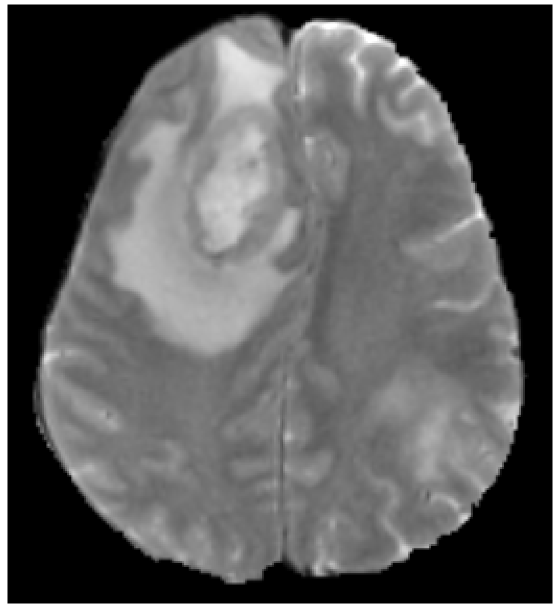
Flair



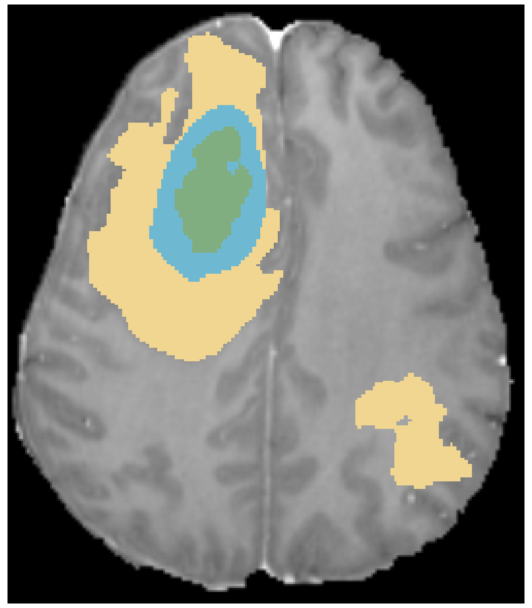
T1



T1CE



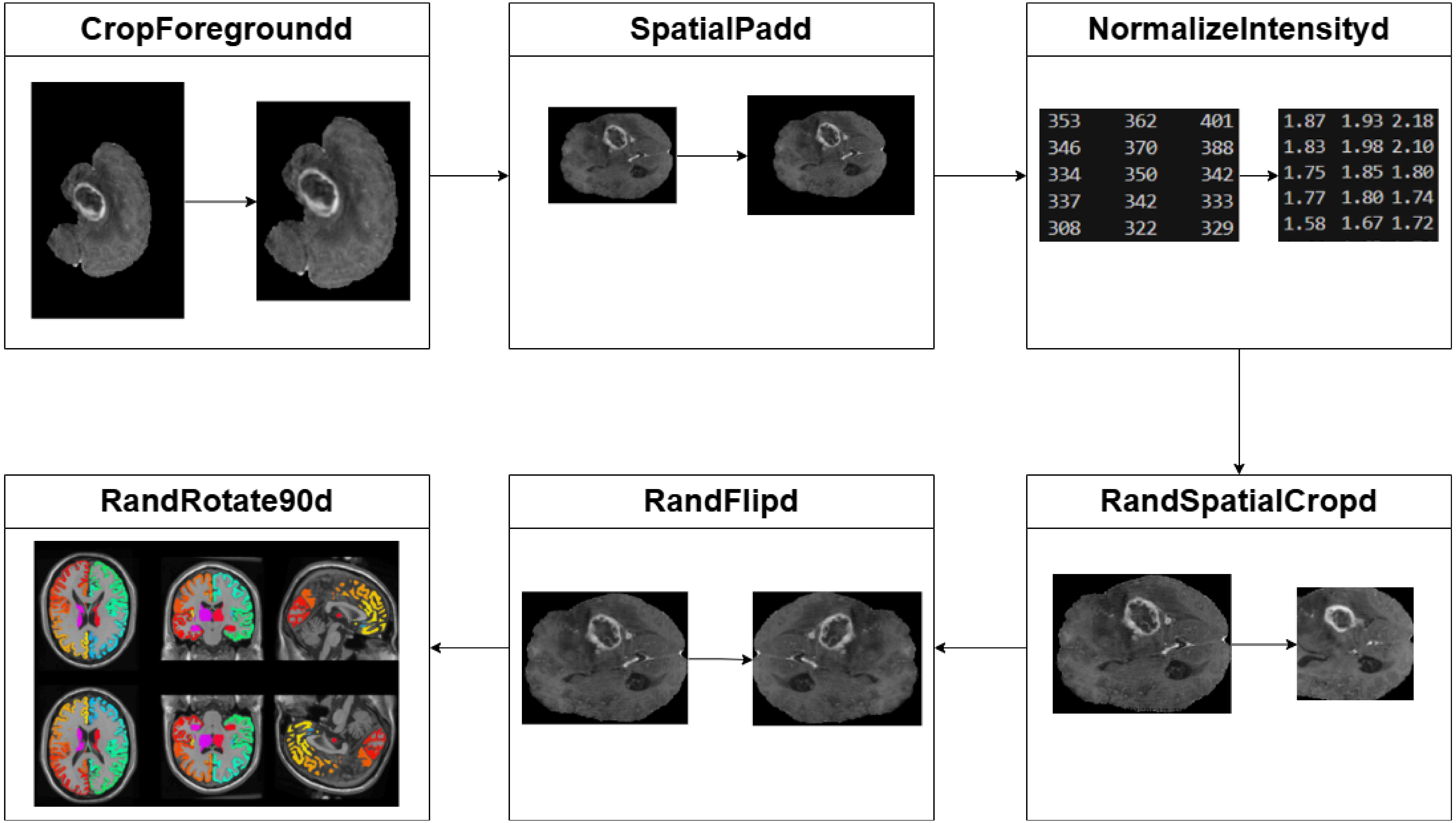
T2



Segment

Methodology

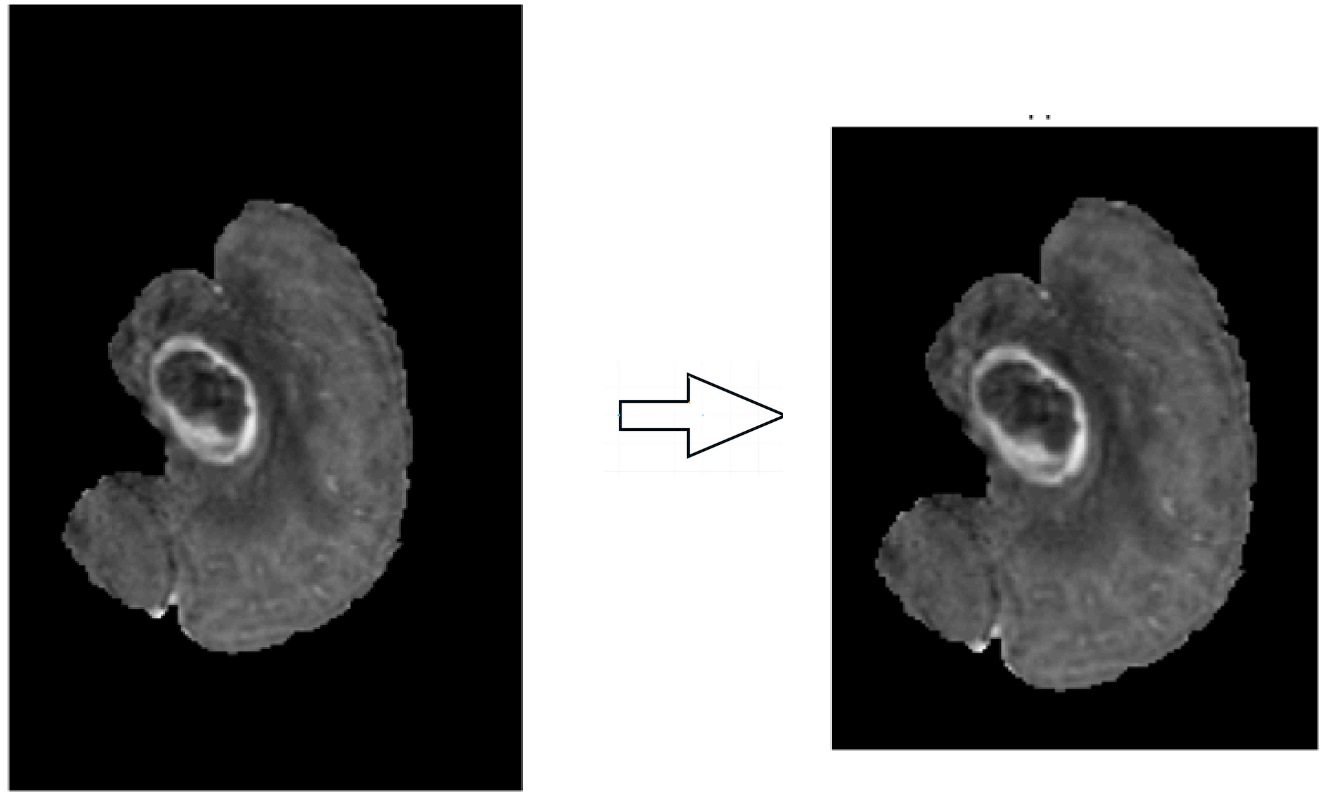
Image processing



Methodology

Image processing - Crop

1.CropForegroundd



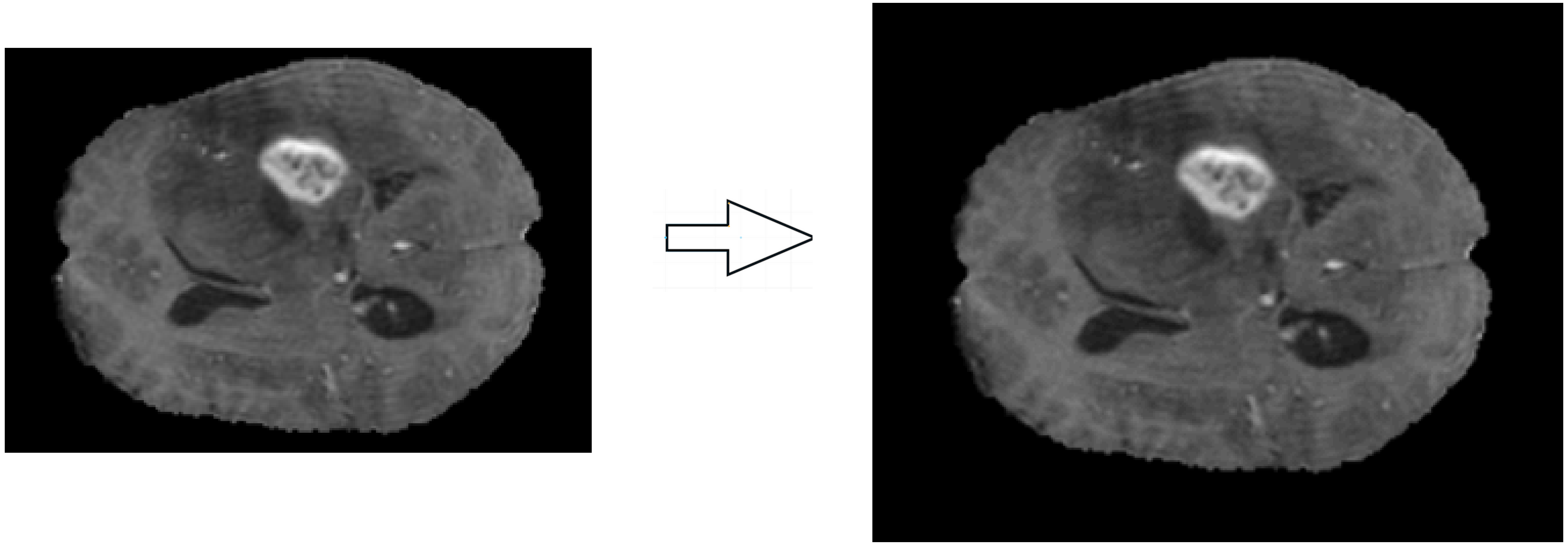
```
Original shape: torch.Size([240, 240, 155])
Cropped shape: torch.Size([240, 173, 135])
```

Crop only the foreground object (the brain) to reduce empty space.

Methodology

Image processing - Padding

2.SpatialPadd



Padding is the process of adding borders to an image to make all images have the same minimum size.

Methodology

Image processing - Normalization

3.NormalizeIntensityd

$$x_{new} = \frac{x - mean}{std}$$

353	362	401	408	364
346	370	388	361	312
334	350	342	341	356
337	342	333	355	365
308	322	329	361	335
320	316	333	360	345
374	352	348	342	337
376	368	356	354	357
381	401	381	357	353
381	394	396	359	345

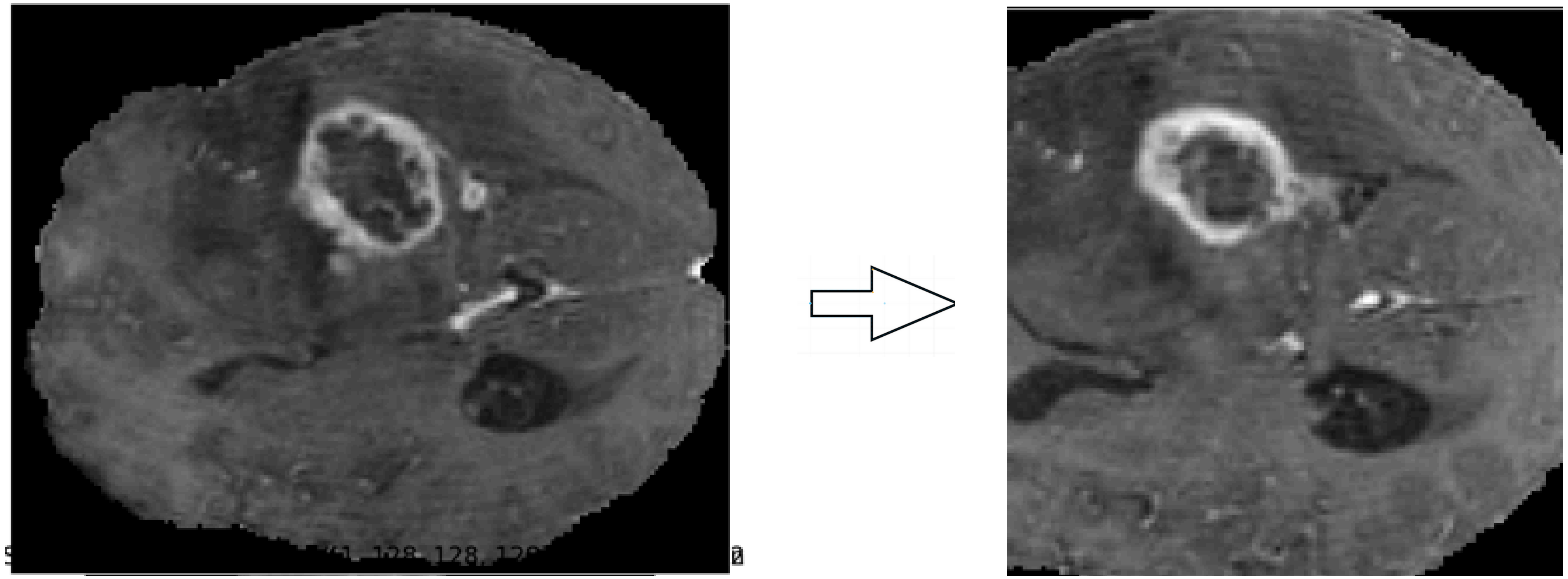
1.87	1.93	2.18	2.23
1.83	1.98	2.10	1.92
1.75	1.85	1.80	1.79
1.77	1.80	1.74	1.88
1.58	1.67	1.72	1.92
1.66	1.63	1.74	1.92
2.01	1.87	1.84	1.80
2.02	1.97	1.89	1.88
2.05	2.18	2.05	1.90
2.05	2.14	2.15	1.91

Normalization helps scale pixel values across all images, reducing intensity variation impact, leading to a more stable and faster learning.

Methodology

Image processing - Random Crop

4.RandSpatialCrop

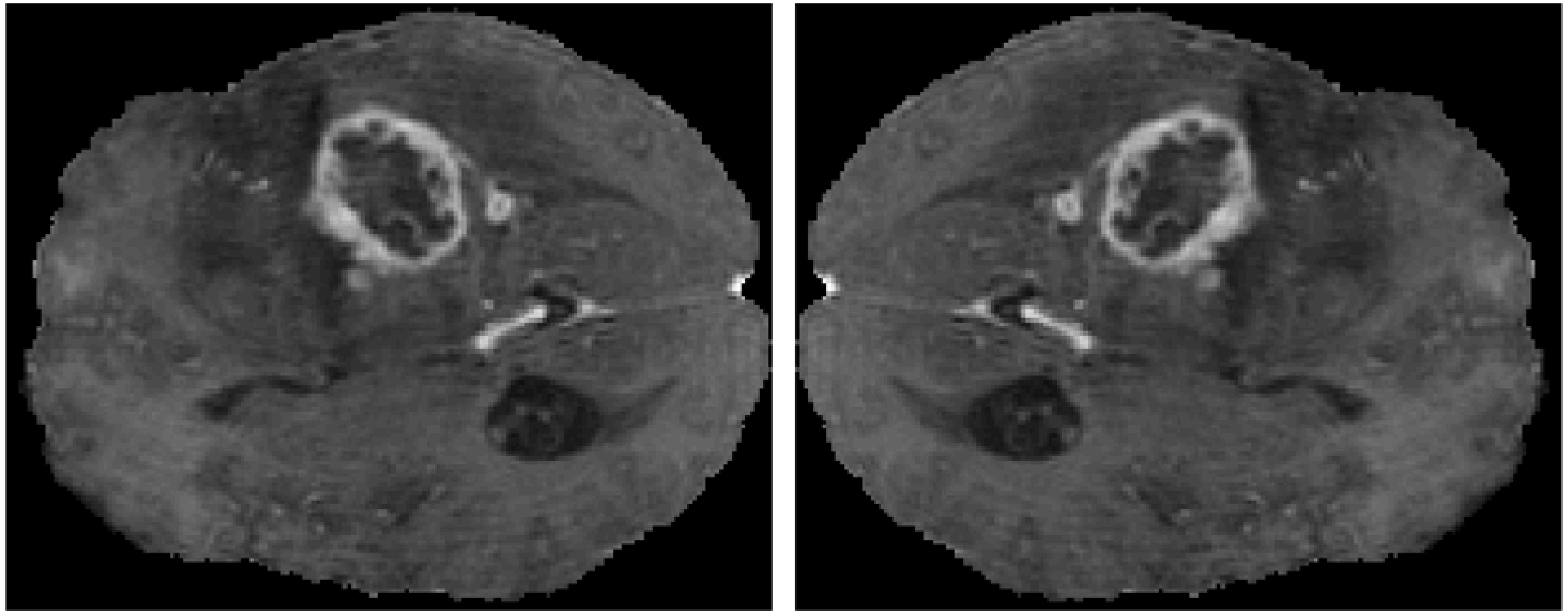


Random Cropping makes all image inputs the same size. The U-Net model needs a fixed input size.

Methodology

Image processing - Flip

5.RandFlipd

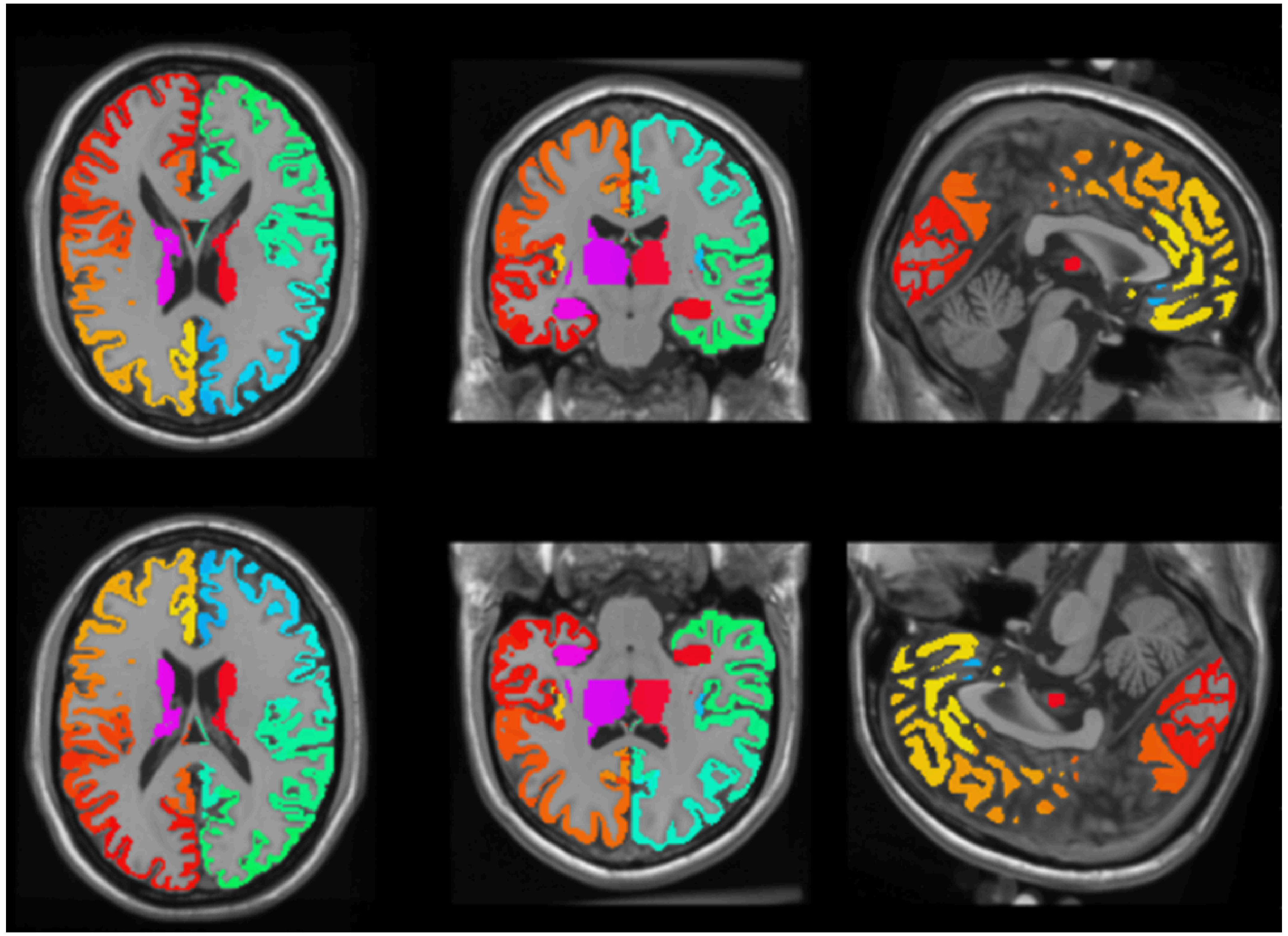


RandFlipd is used to randomly flip the images to augment the training data.

Methodology

Image processing - Rotation

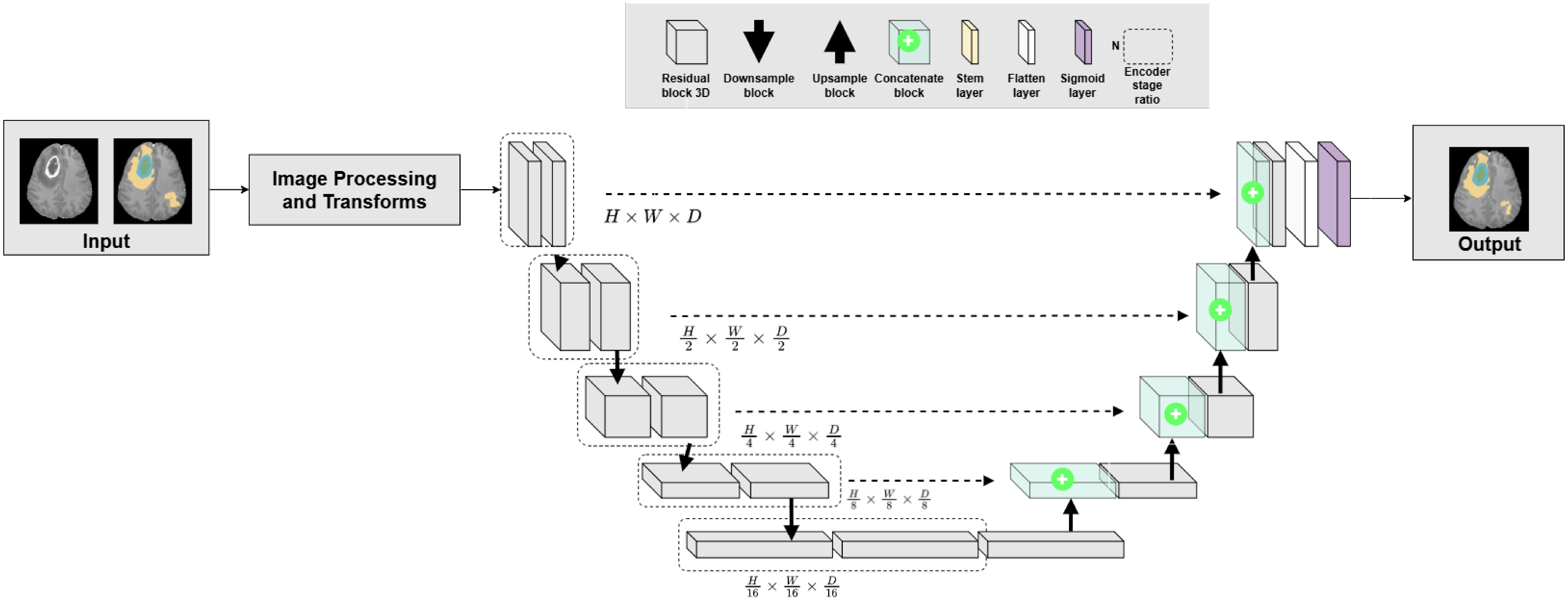
6.RandRotate90d



RandRotate90d randomly rotates the 3D volume by 90° for data augmentation.

Methodology

3DU-Net Model

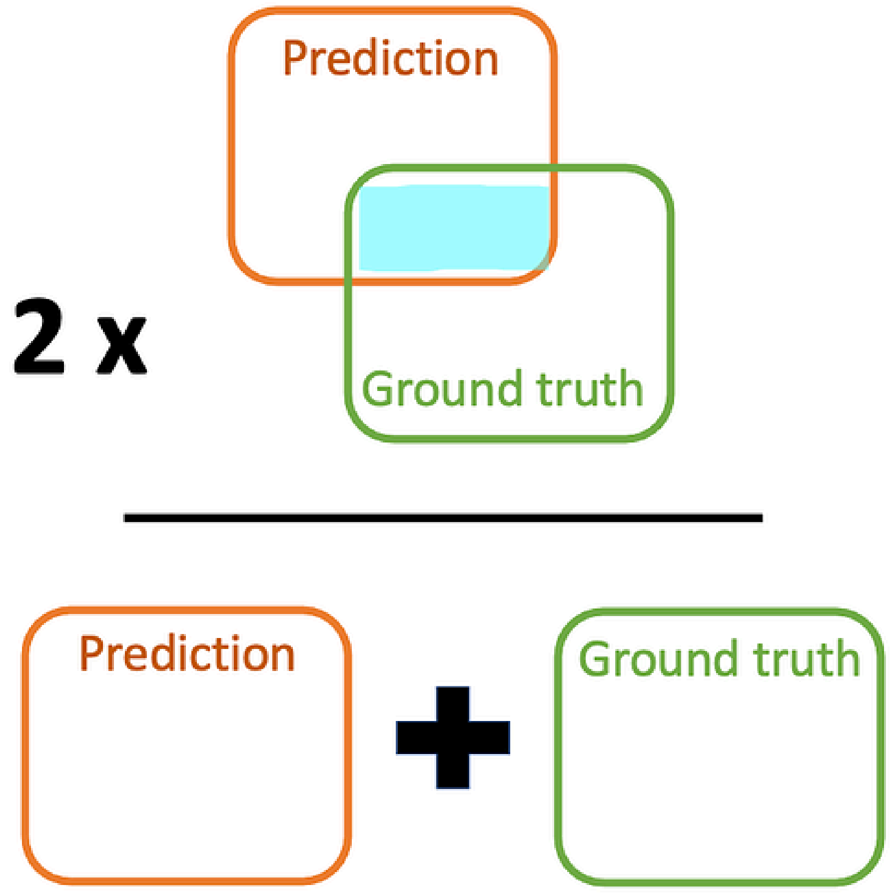


3D-UNet

Evaluations

Dice score coefficient

$$\text{Dice} = \frac{2\ X\ Area\ of\ overlap}{Total\ area} =$$

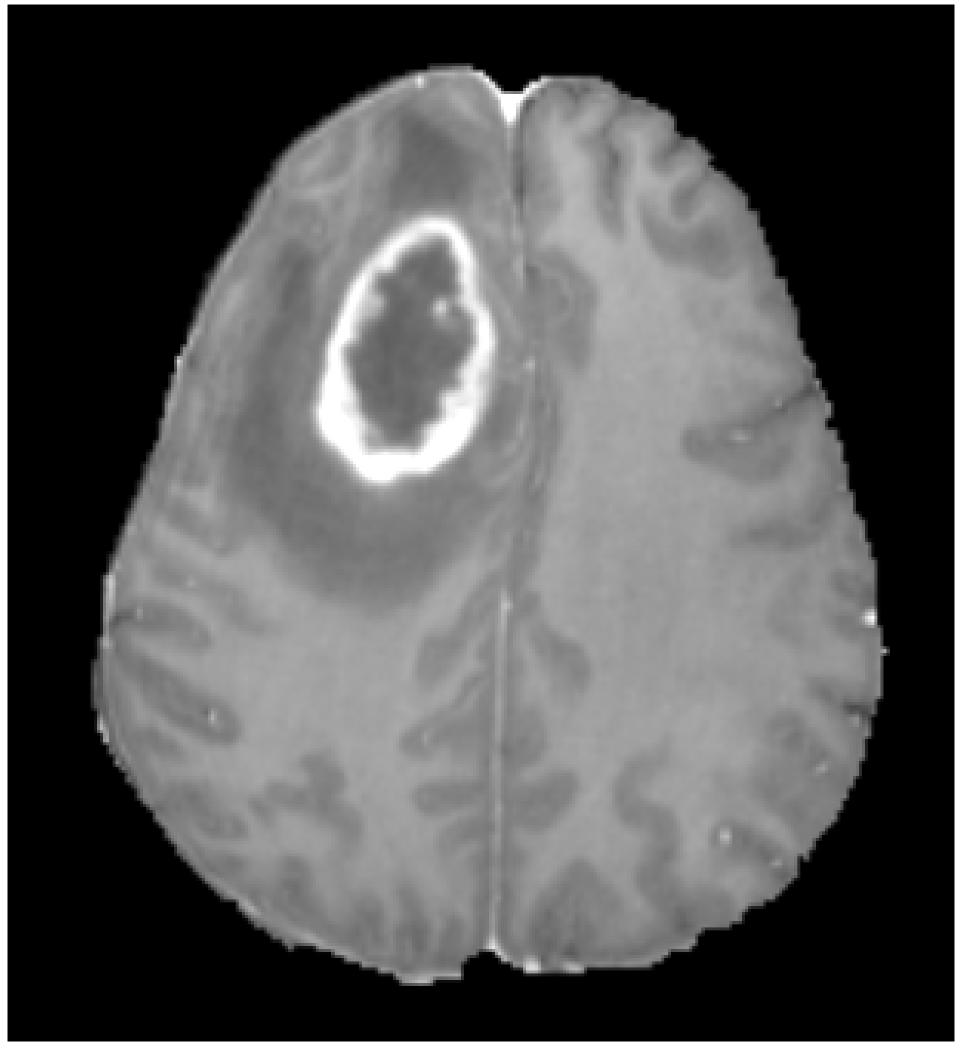


DSC is the main quantitative metric used to measure the spatial overlap between the model's prediction (P) and the Ground Truth segmentation (G). It ranges from 0 (no overlap) to 1 (perfect overlap).

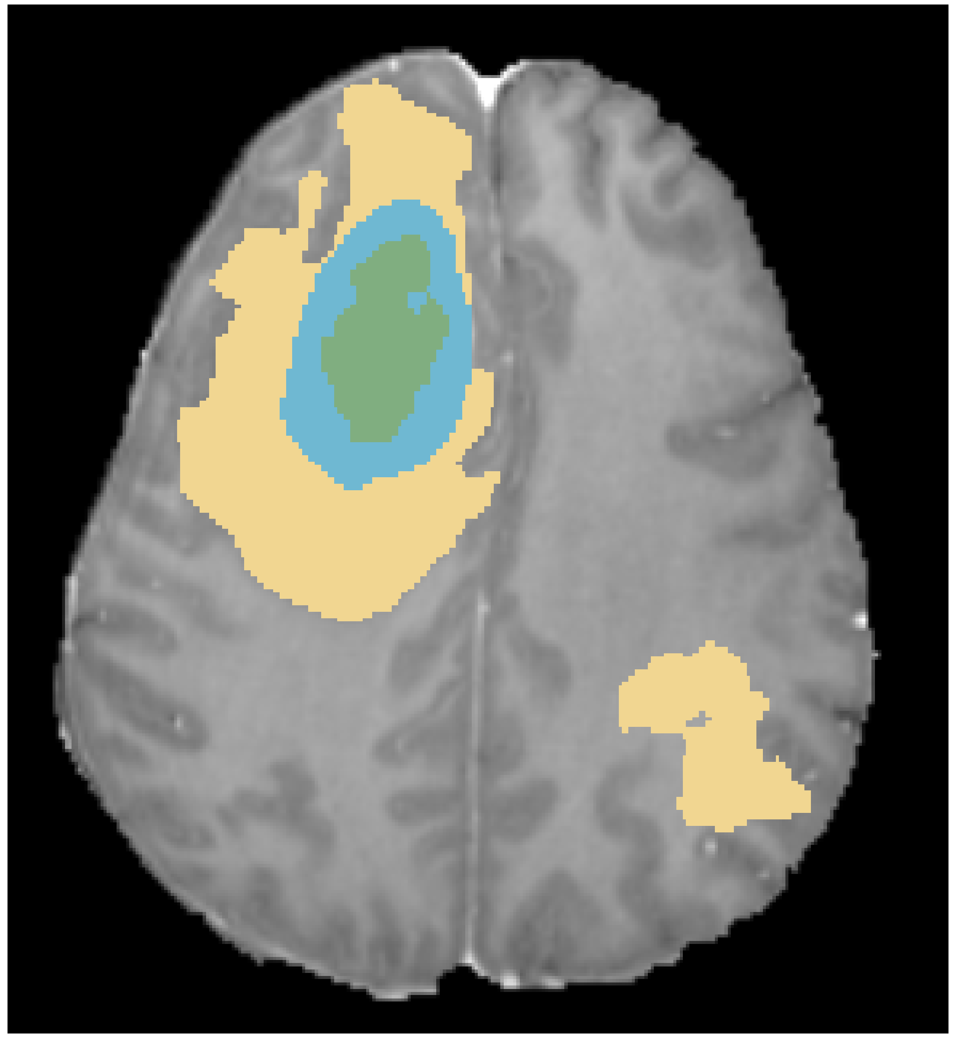
Result

Image result

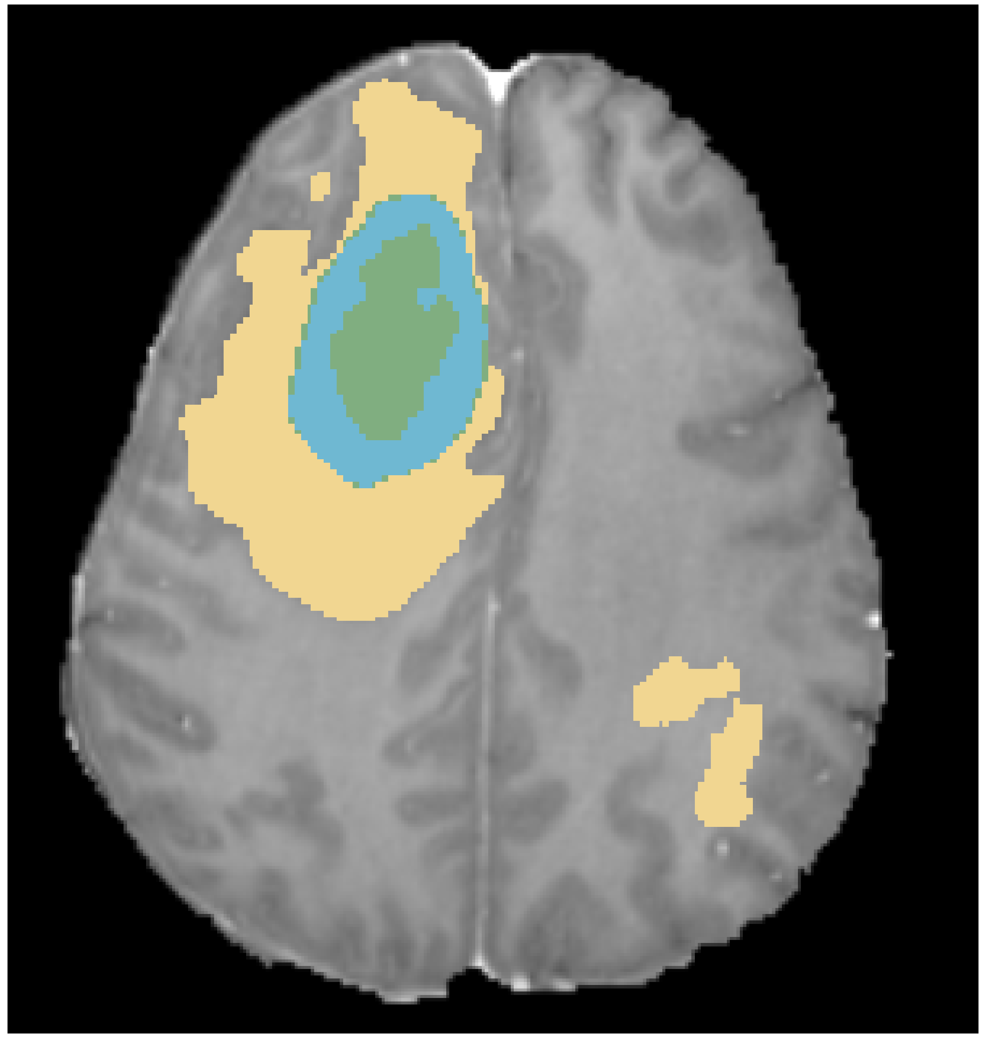
Input



Labels



Predict



Result

Compare Table

Metric	Input 128×128×128 Voxel	Input 96×96×96 Voxel
Val Mean Dice	0.7926	**0.8171**
Val Loss	0.2225	**0.1986**
Train Loss	**0.1595**	0.2078
Dice TC	0.7610	**0.8069**
Dice WT	0.8654	**0.8759**
Dice ET	0.7515	**0.7687**
Time (sec) per picture	1.43	**1.35**

Discussion

- Superior Performance: The 96x96x96 Voxel patch achieved a **Mean Dice Score (DSC) of 0.8171, significantly outperforming the 128x128x128 patch (0.7926)**.
- Class Imbalance: Increasing patch size diluted the density of the tumor Region of Interest (ROI) relative to the background, worsening the Class Imbalance problem and hindering generalization.
- Optimal Balance: The 96x96x96 size provides the Optimal Trade-off, ensuring sufficient global Context Coverage while maximizing Tumor ROI Density for effective feature extraction.

Conclusion

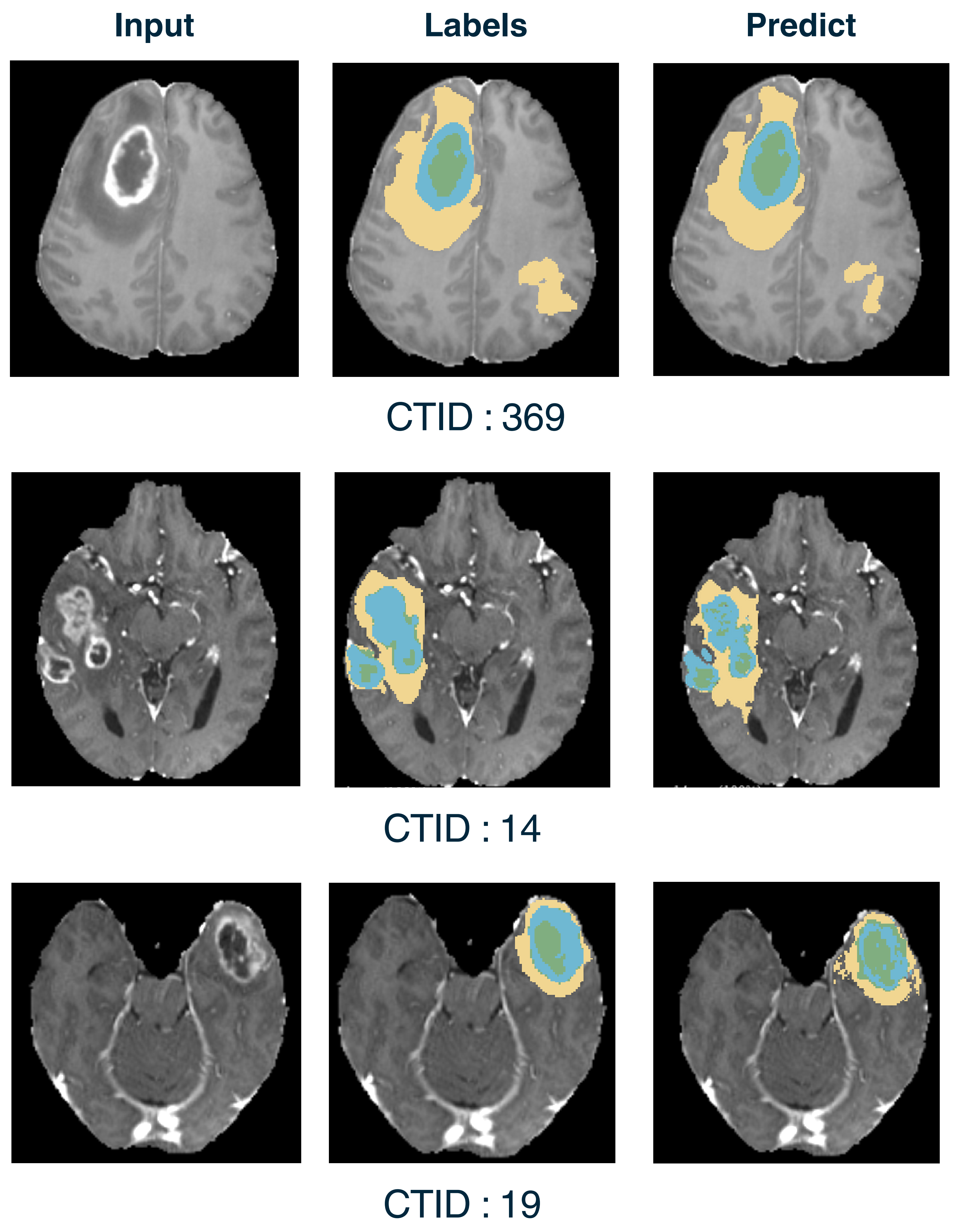
- The selection of Input Patch Size is a critical hyperparameter for 3D medical segmentation tasks.
- The 96x96x96 Voxel dimension is the Optimal Trade-off size for U-Net on the BraTS 2020 dataset, yielding superior Generalization and the highest DSC score.

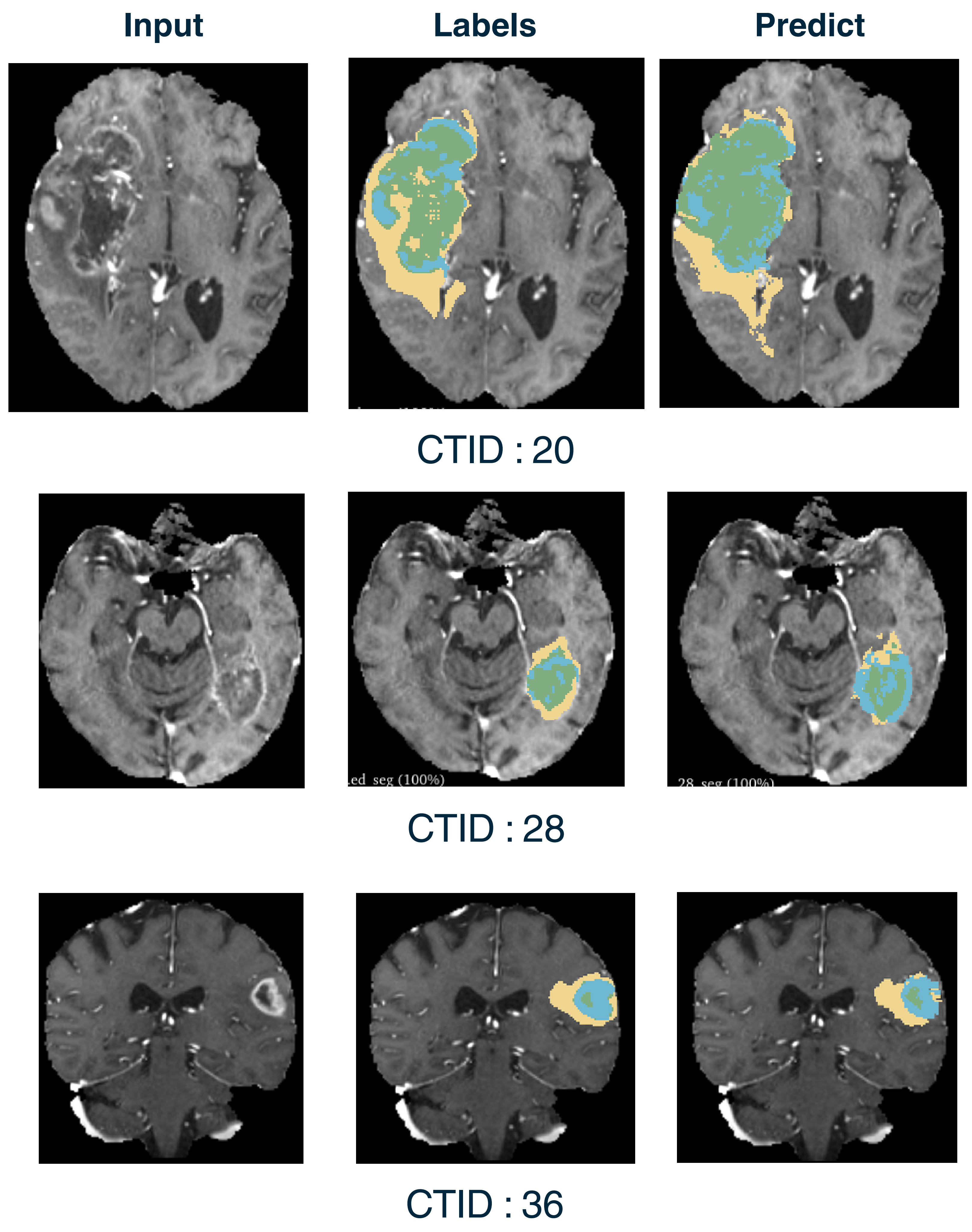
Thank You

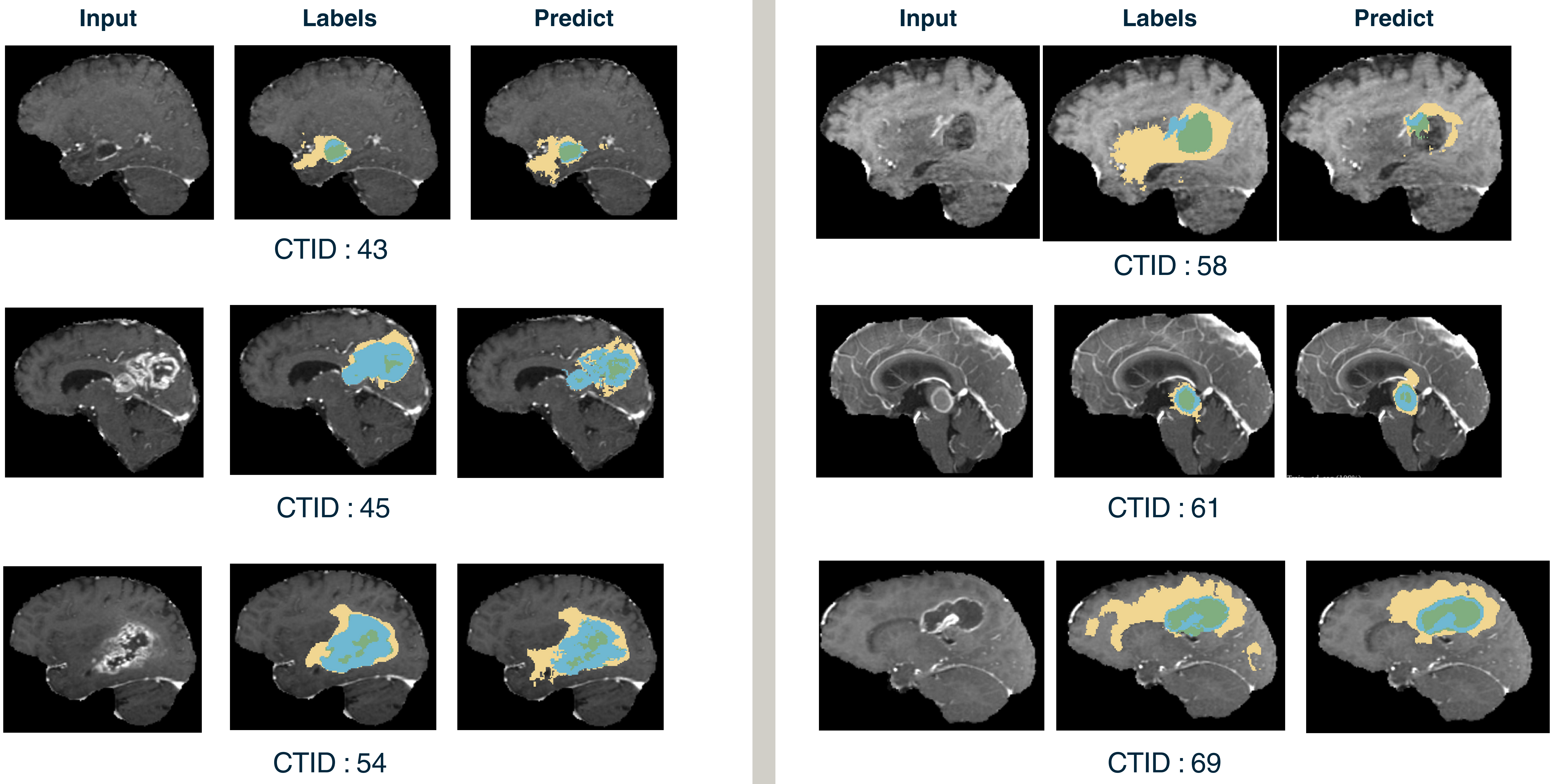
For listening to our presentation

Appendix

Result pictures


Input
Labels
Predict
CTID : 369
CTID : 14
CTID : 19


Input
Labels
Predict
CTID : 20
CTID : 28
CTID : 36


Input
Labels
Predict
CTID : 43
CTID : 45
CTID : 54
Input
Labels
Predict
CTID : 58
CTID : 61
CTID : 69